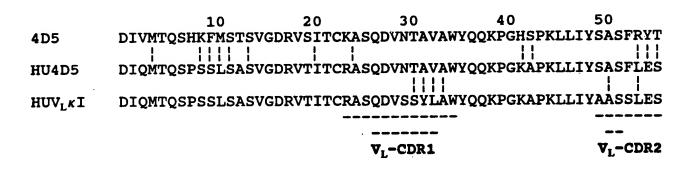
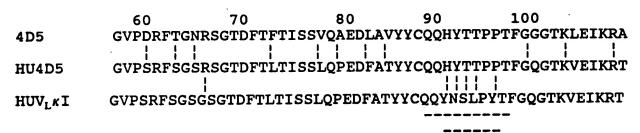
FIGURE 1A: V_L DOMAIN





V_L-CDR3

FIGURE 1B: $\mathbf{V}_{\mathbf{H}}$ DOMAIN

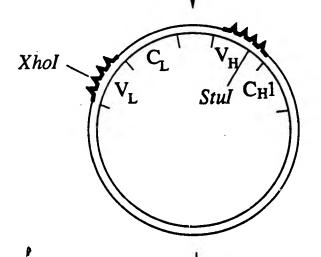
	10	20	30	40	50	A
4D5	EVQLQQSGPELVK	PGASLKLSCTA:	SGFNIKDTYI:	HWVKQRPEQG	LEWIGRI	YPTN
					1 1	
HU4D5	EVQLVESGGGLVQ	PGGSLRLSCAA:	SGFNIKDTYI:	HWVRQAPGKG	LEWVARI	YPTN
				1		
$\mathtt{HUV_{H}III}$	EVQLVESGGGLVQI	PGGSLRLSCAAS	SGFTFSDYAMS	SWVRQAPGKG	LEWVAVIS	ENG
				-		
					•	
			V_H -CDR1		AH-C	DR2

	60	70	80	ABC	90	100ABC
4D5	GYTRYDPKFQD	KATITADTS	SNTAYLQ	VSRLTSE	DTAVYYCS	RWGGDGFYAMDYW
	11111		-			1
HU4D5	GYTRYADSVKG	RFTISADTS	KNTAYLQ	MNSLRAE	DTAVYYCS	RWGGDGFYAMDVW
			<u> </u>			
HUV_HIII	SDTYYADSVKG	RFTISRDDS	KNILTATÖ	MNSLRAE	DTAVYYCAI	RDRGGAVSYFDVW
		•				
						V _u -CDR3

FIGURE 2

Anneal huV_L or huV_H oligomers to pAK1 template

- 1. Ligate
- 2. Isolate assembled oligomers
- 3. Anneal to pAK1 template (XhoI-, StuI+)
- 4. Extend and ligate



- 1. Transform E. coli
- 2. Isolate phagemid pool
- 3. Enrich for huV_L and $huV_H(Xho\ I^+, StuI^-)$
- 4. Sequence verify

